

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Evans, Ronald M.  
No, David

(ii) TITLE OF INVENTION: HORMONE-MEDIATED METHODS FOR MODULATING  
EXPRESSION OF EXOGENOUS GENES IN MAMMALIAN SYSTEMS, AND  
PRODUCTS RELATED THERETO

(iii) NUMBER OF SEQUENCES: 18

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Gray Cary Ware & Freidrich LLP  
(B) STREET: 4365 Executive Drive, Suite 1600  
(C) CITY: San Diego  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 92121-2189

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/974,530  
(B) FILING DATE: November 19, 1997  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter, Stephen E.  
(B) REGISTRATION NUMBER: 31,192  
(C) REFERENCE/DOCKET NUMBER: SALK1520-2

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-677-1409  
(B) TELEFAX: 619-677-1465

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa  
 1        5        10        15

Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa  
 20        25        30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 35        40        45

Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa  
 50        55        60

Lys Cys Xaa Xaa Xaa Gly Met  
 65        70

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Gly Cys Lys Gly  
 1        5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ser Cys Lys Val  
 1            5

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2241
- (D) OTHER INFORMATION: /product = "VgEcR"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATC CCC CCC CGG ACC GAT CTC ACC CTC CGG GAC GAC CTC CAC TTA GAC    48  
 Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
 1        5        10        15

GCC CAC CAC GTC CGG ATC CGG CAT GCC GAC CGG CTA GAC GAT TTC GAT    96  
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
 20        25        30

CTG GAC ATG TTC CGG GAC CGG CAT TCC CGG CGT CGG CGA TTT ACC CCC    144  
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
 35        40        45

CAC GAC TCC CCC CCC TAC CGG GCT CTG GAT ATG CCC GAC TTC GAG TTT    192  
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
 50        55        60

GAG CAG ATC TTT ACC GAT GCC CTT GCA ATT GAC GAG TAC GGT CGG AAC    240  
 Glu Glu Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys  
 65        70        75        80

CTT CTA CGT ACC TCT AGA ACC ATA TCG AAT TCT ATA TCT TCA CGT CGG    288  
 Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg  
 85        90        95

GAT GAT CTC TCG CCT TCG ACC ACC TTG AAC GGA TAC TCG CGG AAC GAA    336  
 Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu  
 100      105      110

ACC TGC GAT CGG AAC AAC ACC AAC AAC GCA CCT CGG CGA CGG CGC GAA    384  
 Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Glu  
 115      120      125

CAG GAG CTC TCC CTC GTC GTC CCC GAC AGG CCC TCC CCC TAC AAC TAC 432  
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
 130 135 140

AAC CCC CTC ACC TGT CGA TCC TCC AAG GTC TTC TTT CCA CCC AGC CTT 480  
 Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val  
 145 150 155 160

ACC AAC ACC GCC GTC TAC TCC TCC AAG TTC CCC CCC GCC TCC GAA ATG 528  
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met  
 165 170 175

GAC ATC TAC ATC AGC CCA AAC TCT CAG GAG TCC CCC CCC CTC AAA AAC TCC 576  
 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Cys Cys  
 180 185 190

CTG CCC CTG CGT ATC CGG CGG GAA TCC GTC GTC CGG GAC AAC CAA TCT 624  
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Glu Cys  
 195 200 205

GCG ATC AAC CGG CGG CAA AAC AAC CCC CAG AAC GAC AAC GAC AAA ATC 672  
 Ala Met Lys Arg Arg Glu Lys Lys Ala Glu Lys Glu Lys Asp Lys Met  
 210 215 220

ACC ACT TCC CGG ACC TCT CAG CAT CGC CCC AAT CCC ACC TTG CCC TCT 720  
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser  
 225 230 235 240

GCT GGC GGC CAA GAC TTT CTT AAC AAC GAC ATT CTT GAC CTT ATG ACA 768  
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
 245 250 255

TCC GAG CGG CCC CAC CAT CCC ACT ATT CCG CTA CTA CCT CAT GAA ATA 816  
 Cys Gln Pro Pro Glu His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
 260 265 270

TTC GGG AAC TCT CAA CGG CCC AAT ATA CCT TCC TTA ACC TAC AAC TAC 864  
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Glu  
 275 280 285

TTC CCC CTT ATA TAC AAG TTA ATT TCC TAC CAG CAT CCC TAT GAC CAG 912  
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln  
 290 295 300

CCA TCT GAA GAG GAT CTC AGG CGT ATA ATC AGT CAA CCC GAT GAC AAC 960  
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn  
 305 310 315 320

GAC AGC CAA ACC GAC GTC ACC TTT CGG CAT ATA ACC GAC ATA ACC ATA 1008  
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
 325 330 335

CTC ACC CTC CAG TTC ATT CTT GAC TTT CCT AAA CCT CTA CCA CCC TTT 1056  
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe  
 340 345 350

ACA AAG ATA CCC CAG GAC GAC CAC ATC ACC TTA CTA AAC CCC TCC TCG 1104  
 Thr Lys Ile Pro Glu Glu Asp Glu Ile Thr Leu Leu Lys Ala Cys Ser  
 355 360 365

TCC GAG CTG ATG ATC CTC CCT ATC GCA CGA CCC TAT GAC CAC AGC TCG 1152  
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
 370 375 380

GAC TCA ATA TTC TTC CCC AAT AAT ACA TCA TAT AGC CCC CAT TCT TAC 1200  
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr  
 385 390 395 400

AAA ATG CCC GCA ATG CCT GAT AAC ATT GAA GAC CTC CTC CAT TTC TCC 1248  
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys  
 405 410 415

CCC CAA ATC TTC TCC ATC AAC CTC GAC AAC CTC GAA TAC CCC CTT CTC 1296  
 Arg Glu Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
 420 425 430

ACT GCC ATT CTC ATC TTC TCC GAC CGG CCC CTC GAC AAC CCC CAA 1344  
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Glu  
 435 440 445

CTA CTC GAA CCC ATC CAC ACC TAC TAC ATC GAC ACC CTA CCC ATT TAT 1392  
 Leu Val Glu Ala Ile Glu Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr  
 450 455 460

ATA CTC AAC CGC CAC TCC GCC GAC TCA ATC ACC CTC CTC TTC TAC GCA 1440  
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
 465 470 475 480

AAC CTC CTC TCC ATC CTC ACC GAC CTC CCT ACC CTC CCC AAC CAC AAC 1488  
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Glu Asn  
 485 490 495

CCC CAG ATG TGT TTC TCA CTA AAG CTC AAA AAC CCC AAA CTC CCC AAC 1536  
 Ala Glu Met Cys Phe Ser Leu Lys Asn Arg Lys Leu Pro Lys  
 500 505 510

TTC CTC GAC GAC ATC TCC GAC CTT CAT CCC ATC CCG CCA TCC GTC CAC 1584  
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Glu  
 515 520 525

TCC CAC CTT CAC ATT ACC CAC GAC GAC AAC CAC CCT CTC GAC CCC CCT 1632  
 Ser His Leu Glu Ile Thr Glu Glu Glu Asn Glu Arg Leu Glu Arg Ala  
 530 535 540

GAC CCT ATG CCC GCA TCC CTT CCC CCC ATT ACC CCC CCC ATT GAT 1680  
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
 545 550 555 560

TCC GAC TCT CCC TCC ACT TCC CCC CCC GCA GCA CCC CCC CCC CAC CAT CAC 1728  
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Glu His Glu  
 565 570 575

CCT CAG CCT CAG CCC CAC CCC CAA CCA CCC TCC TCC CTC ACC CAG AAC GAT 1776  
 Pro Gln Pro Gln Pro Gln Pro Gln Ser Ser Leu Thr Gln Asn Asp  
 580 585 590

TCC CAG CAC CAG ACA CAC CCC CAG CTA CAA CCT CAG CTA CCA CCT CAC 1824  
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln  
 595 600 605

CTC CAA CGT CAA CTC CAA CCC CAG CTC CAA CCA CAG CTT CAC ACG CAA 1872  
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC CTT CCC CTC TCC CCT 1920  
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
 625 630 635 640

CCC CTG CCC GCC TCC CTA ACC GCA CCT CGT TCC TTG TCC CCC GTC ACT 1968  
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
 645 650 655

ACC ACC ACC GAA TAC ATG CCC GGA ACT GGC GGC ATA GCA CCC ATC ACC 2016  
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
 660 665 670

CCC GCA ACC ACC ACC AGT ATC ACC CCT CCC GTT ACC CCT ACC TCC ACC 2064  
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
 675 680 685

ACA TCA CGG GTC ATG CCC AAC GCA CTT GGA CTC CCT CCT GTC CGG GTC 2112  
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
 690 695 700

CCC CCC AAC GTC ACC ATG TAT GGC AAC CCC CAC ACC CCC ATC CCC TTC 2160  
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
 705 710 715 720

ATG CGT GTC GCA CCC CTC CAT TCG CAC CAA CAC CAG CAC CTT ATC CCC GCA CTC 2208  
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val  
 725 730 735

CCC GTT AAG TCG GAC CAC TCG ACC ACT GCA TAG 2241  
 Ala Val Lys Ser Glu His Ser Thr Thr Ala  
 740 745

## (2) INFORMATION FOR SEQ ID NO:5:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: protein

### (iii) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
 1        5        10        15

Gly Glu Asp Val Ala Met Ala Ile Ala Asp Ala Leu Asp Asp Phe Asp  
 20        25        30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
 35        40        45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
 50        55        60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys  
 65        70        75        80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg  
 85        90        95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu  
 100      105      110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln  
 115      120      125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
 130      135      140

Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val  
 145      150      155      160

Tyr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met  
 165      170      175

Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys  
 180      185      190

Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Glu Cys  
 195      200      205

Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met  
 210      215      220

Tyr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser  
 225      230      235      240

Gly Gly Gly Glu Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
 245      250      255

Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
 260      265      270

Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln  
 275      280      285

Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln  
 290      295      300

Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn  
 305            310            315            320

Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
 325            330            335

Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe  
 340            345            350

Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser  
 355            360            365

Ser Gln Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
 370            375            380

Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr  
 385            390            395            400

Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys  
 405            410            415

Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
 420            425            430

Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln  
 435            440            445

Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr  
 450            455            460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
 465            470            475            480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn  
 485            490            495

Ala Gln Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
 500            505            510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln  
 515            520            525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala  
 530            535            540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
 545            550            555            560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln  
 565            570            575

Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp  
 580            585            590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln

595        600        605

Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
 610        615        620

Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
 625        630        635        640

Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
 645        650        655

Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
 660        665        670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
 675        680        685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
 690        695        700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
 705        710        715        720

Met Gly Val Ala Leu His Ser His Gln Gln Leu Ile Gly Gly Val  
 725        730        735

Ala Val Lys Ser Glu His Ser Thr Thr Ala  
 740        745

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2241
- (D) OTHER INFORMATION: /product = "VpEcR"

(iv) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG CCC CCC CGG ACC CAT GTC ACC CTG CGG GAC GAG CTC CAC TTA GAC     48  
 Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
 1        5        10        15

GCC GAC GAC GTC CCC ATG CGG CAT CCC GAC GCG CTA GAC GAT TTC GAT     96  
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
 20        25        30

CTC GAC ATC TTG CCC GAC GGG GAT TCC CCC CCT CGG GCA TTT ACC CCC 144  
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Phe Thr Pro  
 35 40 45

CAC GAC TCC CCC CCC TAC GGC CCT CTG GAT ATG CCC GAC TTC GAC TTT 192  
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
 50 55 60

GAC CAC ATG TTT ACC GAT GGC CTT CGA ATT GAC GAC TAC CCT CGG AAC 240  
 Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Lys  
 65 70 75 80

CTT CTA CGT ACC TCT AGA ACC ATA TCG AAT TCT ATA TCT TCA CCT CCC 288  
 Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg  
 85 90 95

GAT GAT CTC TCC CCT TCC ACC ACC TTC AAC GCA TAC TCC GGC AAC GAA 336  
 Asp Asp Leu Ser Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu  
 100 105 110

ACC TCC GAT CCC AAC AAC ACC AAC GAG GCA CCT CCC CCA CCC CTC CAA 384  
 Ser Cys Asp Ala Lys Lys Ser Lys Gly Pro Ala Pro Arg Val Gln  
 115 120 125

CAC GAG CTC TCC CTC GTT TCC GGC GAC ACC GGC TCC CCC TAC CAC TAC 432  
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
 130 135 140

AAC CCC CTC ACC TGT CAG CCC TCC AAG GGG TTC TTT CGA CCC ACC GTT 480  
 Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val  
 145 150 155 160

ACG AAG ACC CCC GTC TAC TCC AAC GTC TCC CCC CCC CCC TCC GAA ATC 528  
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met  
 165 170 175

GAC ATC TAC ATG ACC CGA AAC AAG TGT CAG GAG TCC CCC CTC AAA AAC TCC 576  
 Asp Met Tyr Met Arg Arg Lys Cys Glu Glu Cys Arg Leu Lys Lys Cys  
 180 185 190

CTG CCC GTG CGT ATG CGG CGG GAA TGC GTC GTC CCC GAC AAC CAA TCT 624  
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys  
 195 200 205

GCC ATC AAG CCC CGG GAA AAC AAG GGC CAC AAC GAC GAC AAC AAA ATC 672  
 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met  
 210 215 220

ACC ACT TCC CCC ACC TCT CAG CAT CCC GGC AAT GGC ACC TTC GGC TCT 720  
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser  
 225 230 235 240

CCT CCC CGG CAA GAC TTT CTT AAC AAC GAC ATT CTT GAC CTT ATC ACA 768  
 Gly Gly Gly Cln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
 245 250 255

TGC GAC CCC CCC CAG CAT CCC ACT ATT CGG CTA CTA CCT GAT GAA ATA 816  
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
 260 265 270

TTC CCC AAC TGT CAA CCC CCC AAT ATA CCT TCC TTA ACC TAC AAT CAG 864  
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln  
 275 280 285

TTC GCC GTT ATA TAC AAC TTA ATT TCG TAC CAG CAT CCC TAT GAG CAC 912  
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln  
 290 295 300

CCA TCT GAA GAG GAT CTC AGG CGT ATA ATC ACT CAA CCC CAT GAC AAC 960  
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn  
 305 310 315 320

CAG ACC CAA ACC GAC GTC AGC TTT CGG CAT ATA ACC GAG ATA ACC ATA 1008  
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
 325 330 335

CTC ACC CTC CAG TTC ATT CTT GAG TTT GCT AAA CGT CTA CCA CCC TTT 1056  
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe  
 340 345 350

ACA AAC ATA CCC CAG CAG CAG CAC ATC ACC TTA CTA AAC GCC TCC TCG 1104  
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser  
 355 360 365

TCC GAC CTG ATG ATG CTG CGT ATG GCA CGA CCC TAT GAC CAC ACC TCG 1152  
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
 370 375 380

GAC TCA ATA TTC TTC GCG AAT AAT AGA TCA TAT ACC CGG GAT TCT TAC 1200  
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr  
 385 390 395 400

AAA ATG GCC GGA ATG CCT CAT AAC ATT GAA GAC CTG CTG CAT TTC TCC 1248  
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys  
 405 410 415

CGC CAA ATG TTC TCC ATG AAC GTC GAC AAC GTC GAA TAC CCC CTT CTC 1296  
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
 420 425 430

ACT CCC ATT CTC ATC TTC TCG GAC ACC TAC TAC ATC GAC ACC CTA CCC ATT TAT 1344  
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln  
 435 440 445

CTA CTC GAA GCG ATC CAG ACC TAC TAC ATC GAC ACC CTA CCC ATT TAT 1392  
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr  
 450 455 460

ATA CTC AAC CCC CAC TCC CCC GAC TCA ATG ACC CTC GTC TTC TAC GCA 1440  
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
 465 470 475 480

AAG CTC CTC TCG ATC CTC ACC GAC CTC CCT ACC CTC CCC AAC CAC AAC 1488  
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Glu Asn  
 485 490 495

GCC GAC ATG TCT TTC TCA CTA AAC CTC AAA AAC CCC AAA CTC CCC AAC 1530  
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
 500 505 510

TTC CTC GAC GAC ATC TGG GAC CTT CAT CCC ATC CCC CCA TGG CTC CAC 1584  
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Glu  
 515 520 525

TCC CAC CCT CAG ATT ACC CAG GAC GAC AAC GAC CCT CTC GAC CCC CCT 1632  
 Ser His Leu Glu Ile Thr Glu Glu Glu Asn Glu Arg Leu Glu Arg Ala  
 530 535 540

GAC CCT ATC CGG GCA TCC CTT CGG CCC CCC ATT ACC CCC CCC ATT CAT 1680  
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
 545 550 555 560

TGC GAC TCT GCC TCC ACT TCG CGG CCC GCA CCC CCC GCG CAC CAT CAC 1728  
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Glu His Glu  
 565 570 575

CCT CAC CCT CAC CCC CAG CCC CAA CCC TCC TCC CTG ACC CAG AAC CAT 1776  
 Pro Glu Pro Glu Pro Glu Pro Glu Pro Ser Ser Leu Thr Glu Asn Asp  
 580 585 590

TCC CAC CAC CAC ACA CAG CCC CAC CTA CAA CCT CAC CTA CCA CCT CAC 1824  
 Ser Glu His Glu Thr Glu Pro Glu Leu Glu Pro Glu Leu Pro Pro Glu  
 595 600 605

CTG CAA GGT CAA CTC CAA CCC CAC CTC CAA CCA CAG CTT CAC ACC CAA 1872  
 Leu Glu Gly Glu Leu Glu Pro Glu Leu Glu Pro Glu Leu Glu Thr Glu  
 610 615 620

CTC CAC CCA CAC ATT CAA CCA CAC CCA CAC CTC CCT CCC CTC TCC CCT 1920  
 Leu Glu Pro Glu Ile Glu Pro Glu Pro Glu Leu Leu Pro Val Ser Ala  
 625 630 635 640

CCC CTG CCC CCC TCC CTA ACC CCA CCT CGT TCC TTC TCC CCC GTC ACT 1968  
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
 645 650 655

ACC ACC ACC GAA TAC ATG CCC CCA AGT CCC CCC ATA GCA CCC ATC ACC 2016  
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
 660 665 670

CCC GCA ACC ACC ACC ACT ATC ACC CCT CCC CTT ACC CCT ACC TCC ACC 2064  
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
 675 680 685

ACA TCA CCC GTA CCA ACC CCC AAC CCA CTT CCA CTC CGT CTT CCC CTC 2112  
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
 690 695 700

GGC CCC AAC GTC ACC ATC TAT GCG AAC GCC CAG ACC CCC ATC CCC TTC 2160  
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Glu Thr Ala Met Ala Leu  
 705 710 715 720

ATG CCT GTC CCC CTC CAT TCC CAC CAA GAC CAG CTT ATC CGG CGA CTC 2208  
 Met Gly Val Ala Leu His Ser Ile His Glu Glu Leu Ile Gly Gly Val  
 725 730 735

GCG CTT AAC TCC GAC CAC TCC ACC ACT GCA TAG 2241  
 Ala Val Lys Ser Glu His Ser Thr Thr Ala  
 740 745

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu Ile Leu Asp  
 1 5 10 15

Gly Glu Asp Val Ala Met Ala Ile Asp Ala Leu Asp Asp Phe Asp  
 20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
 35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
 50 55 60

Glu Cln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys  
 65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg  
 85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu  
 100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Glu  
 115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr Ile Tyr  
 130 135 140

Asn Ala Leu Thr Cys Glu Cys Cys Lys Gly Phe Phe Arg Arg Ser Val  
 145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met

165            170            175

Asp Met Tyr Met Arg Arg Lys Cys Glu Glu Cys Arg Leu Lys Lys Cys  
 180            185            190

Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Glu Cys  
 195            200            205

Ala Met Lys Arg Arg Glu Lys Lys Ala Glu Lys Glu Lys Asp Lys Met  
 210            215            220

Thr Thr Ser Pro Ser Ser Glu His Gly Gly Asn Gly Ser Leu Ala Ser  
 225            230            235            240

Gly Gly Gly Glu Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
 245            250            255

Cys Glu Pro Pro Glu His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
 260            265            270

Leu Ala Lys Cys Glu Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Glu  
 275            280            285

Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Glu Asp Gly Tyr Glu Glu  
 290            295            300

Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Glu Pro Asp Glu Asn  
 305            310            315            320

Glu Ser Glu Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
 325            330            335

Leu Thr Val Glu Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe  
 340            345            350

Thr Lys Ile Pro Glu Glu Asp Glu Ile Thr Leu Leu Lys Ala Cys Ser  
 355            360            365

Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
 370            375            380

Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr  
 385            390            395            400

Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys  
 405            410            415

Arg Glu Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
 420            425            430

Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Glu  
 435            440            445

Leu Val Glu Ala Ile Glu Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr  
 450            455            460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
 465            470            475            480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn  
 485            490            495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
 500            505            510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln  
 515            520            525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala  
 530            535            540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
 545            550            555            560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln  
 565            570            575

Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp  
 580            585            590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln  
 595            600            605

Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
 610            615            620

Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
 625            630            635            640

Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
 645            650            655

Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
 660            665            670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
 675            680            685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
 690            695            700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
 705            710            715            720

Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val  
 725            730            735

Ala Val Lys Ser Glu His Ser Thr Thr Ala  
 740            745

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (iii) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3126
- (D) OTHER INFORMATION: /product = "CEcr"

## (iv) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GAC TCC AAA GAA TCA TTA ACT CCT GGT AGA GAA GAA AAC CCC ACC 48  
 Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser  
 1 5 10 15

ACT CTC CTT CCT CAC CAC ACC CGA CAT GTC ATC GAC TTC TAT AAA ACC 96  
 Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr  
 20 25 30

CTA ACA CGA CGA CCT ACT GTC AAC GTC TCT TCT TCA CGG TCA CTC 144  
 Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu  
 35 40 45

GCT CTC CCT TCT CAA TCA CAC TCC AAC CAG CGA AGA CTT TTC GTT CAT 192  
 Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp  
 50 55 60

TTC CGA AAA CGC TCA CTA ACC AAT CGC CAG CAG CGA CAT CTC TCC AAA 240  
 Phe Pro Lys Gly Ser Val Ser Asn Ala Cln Cln Pro Asp Leu Ser Lys  
 65 70 75 80

CGA CTT TCA CTC TCA ATG CGA CTC TAT ATG CGA GAC ACA GAA ACA AAA 288  
 Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys  
 85 90 95

GTC ATG CGA AAT GAC CTC CGA TTC CGA CAG CAG CGC CAA ATC ACC CTT 336  
 Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gln Ile Ser Leu  
 100 105 110

TCC TCC CGG GAA ACA GAC TTA AAC CTT TTC GAA GAA ACC ATT CGA AAC 384  
 Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn  
 115 120 125

CTC AAT AGG TCC ACC ACT GTT CGA GAG AAC CGC AAC AAC ACT TCA CGA TCC 432  
 Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser  
 130 135 140

ACT CCT CTG TCT CCT GCC CCC ACA GAC AAC GAC TTT CCA AAA ACT CAC 480  
 Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His  
 145 150 155 160

TCT GAT GTC TUT TCA GAA CAG CAA CAT TTC AAG CCC CAG ACT CCC ACC 528  
 Ser Asp Val Ser Ser Glu Glu His Leu Lys Glu Glu Thr Gly Thr  
 165 170 175

AAC CCT CCC AAT CTC AAA TTC TAT ACC ACA GAC CAA ACC ACC TTT CAC 576  
 Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Glu Ser Thr Phe Asp  
 180 185 190

ATT TTG CAG GAT TTC GAG TTT TCT TGT GGG TCC CCA CCT AAA GAC ACC 624  
 Ile Leu Glu Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr  
 195 200 205

AAT GAC ACT CCT TGC AGA TCA CAC CTC TTC ATA GAT CAA AAC TCT TTC 672  
 Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu  
 210 215 220

CTT TCT CCT CTC CCC CGA GAA GAC GAT TCA TTC CTT TTG CAA CGA AAC 720  
 Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn  
 225 230 235 240

TCC AAT GAC GAC TCC AAC CCT CTC ATT TTA CGG GAC ACT AAA CCC AAA 768  
 Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys  
 245 250 255

ATT AAC GAT AAT CGA GAT CTC GTT TTC TCA ACC CCC ACT AAT CTA ACA 816  
 Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr  
 260 265 270

CTC CCC CAA GTG AAA ACA GAA AAA GAA GAT TTC ATC CAA CTC TCC ACC 864  
 Leu Pro Glu Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr  
 275 280 285

CCT CCC GTA ATT AAC CAA GAC AAA CTC CCC ACA CTT TAC TGT CAC CGA 912  
 Pro Glu Val Ile Lys Glu Glu Lys Leu Gly Thr Val Tyr Cys Glu Ala  
 290 295 300

ACC TTT CCT CGA GCA AAT ATA ATT CCT AAT AAA ATG TCT GCC ATT TCT 960  
 Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser  
 305 310 315 320

GTT CAT CGT GTC ACT ACC TCT CGA CGA CAG ATG TAC CAC TAT GAC ATG 1008  
 Val His Gly Val Ser Thr Ser Gly Gly Glu Met Tyr His Tyr Asp Met  
 325 330 335

AAT ACA GCA TCC CCT CCT CAA CAA CAG CAG CAT CAG AAC CCT ATT TTT AAT 1056  
 Asn Thr Ala Ser Leu Ser Glu Glu Asp Glu Lys Pro Ile Phe Asn  
 340 345 350

GTC ATT CGA CGA ATT CCC CTT CCT CGA AAT TCC AAT ACC TCC CGA 1104  
 Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Glu  
 355 360 365

GCA TCT GCA GAT GAC AAC TTG ACT TCT CTC GGG ACT CTC AAC TTC CCT 1152  
 Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro  
 370 375 380

GCT CGA ACA GTT TTT TCT AAT CCC TAT TCA ACC CCC ACC ATC ACA CCA 1200  
 Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro  
 385 390 395 400

GAT GTC ACC TCT CCT CCA TCC ACC TCC TCA ACA GCA ACA ACA GCA CCA 1248  
 Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro  
 405 410 415

CCT CCC ACC CCC CCC GTC CAA GAC GAG CTC TCC CTC CTT TCC CCC GAC 1296  
 Pro Pro Ser Gly Arg Val Glu Glu Leu Cys Leu Val Cys Gly Asp  
 420 425 430

ACC GCC TCC CCC TAC CAC TAC AAC GCC CTC ACC TCT GCA TCC TCC AAC 1344  
 Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys  
 435 440 445

GTC TTC TTT CCA CGG ACC GTT ACC AAC ACC CCC GTC TAC TCC TCC AAC 1392  
 Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys  
 450 455 460

TTC GGG CCC CCC TCC CAA ATC GAC ATC TAC ATC ACC GCA AAC TCT CAG 1440  
 Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Glu  
 465 470 475 480

CAG TCC CCC CTC AAA AAG TCC CTC CCC CTC CCT ATC CCC CCC GAA TCC 1488  
 Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys  
 485 490 495

GTC GTC CCC GAG AAC CAA TGT CGG ATC AAC CGG CCC CCG CAA AAC AAC CCC 1536  
 Val Val Pro Glu Asn Glu Cys Ala Met Lys Arg Arg Glu Lys Lys Ala  
 500 505 510

CAC AAC CAG AAC GAC AAA ATG ACC ACT TCC CCC ACC TCT CAG CAT CCC 1584  
 Glu Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Glu His Gly  
 515 520 525

GCC AAT CGG AGC TTG GCC TCT CCT CGG CCC CAA GAC TTT CTT AAC AAG 1632  
 Gly Asn Gly Ser Leu Ala Ser Gly Gly Glu Asp Phe Val Lys Lys  
 530 535 540

CAG ATT CTT GAC CTT ATG ACA TCC GAG CCC CCC CAC CAT CCC ACT ATT 1680  
 Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Glu His Ala Thr Ile  
 545 550 555 560

CGG CTA CTA CCT GAT GAA ATA TTG GCC AAG TGT CAA CGG CCC AAT ATA 1728  
 Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Glu Ala Arg Asn Ile  
 565 570 575

CCT TCC TTA ACC TAC AAT CAG TTG GCC AAG TGT CAA CGG CCC AAT ATA 1776  
 Pro Ser Leu Thr Tyr Asn Glu Leu Ala Val Ile Tyr Lys Leu Ile Trp  
 580 585 590

TAC CAG GAT CCC TAT GAG CAG CCA TCT GAA GAG GAT CTC AGG CGT ATA 1824  
 Tyr Glu Asp Gly Tyr Glu Glu Pro Ser Glu Glu Asp Leu Arg Arg Ile  
 595 600 605

ATC ACT CAA CCC GAT GAG AAC GAG ACC CAA ACC GAC CTC AGC TTT CCG 1872  
 Met Ser Glu Pro Asp Glu Asn Glu Ser Glu Thr Asp Val Ser Phe Arg  
 610 615 620

CAT ATA ACC GAG ATA ACC ATA CTC ACC GTC CAG TTC ATT CTT GAC TTT 1920  
 His Ile Thr Glu Ile Thr Ile Leu Thr Val Glu Leu Ile Val Glu Phe  
 625 630 635 640

GCT AAA CCT CTA CCA CCC TTT ACA AAG ATA CCC CAC GAG GAC CAG ATC 1968  
 Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Glu Glu Asp Glu Ile  
 645 650 655

ACG TTA CTA AAG GCC TGC TCG TCC GAG GTG ATC ATC CTG CGT ATG GCA 2016  
 Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala  
 660 665 670

CGA CCC TAT GAC CAC ACC TCG GAC TCA ATA TTC TTC CGG AAT AAT ACA 2064  
 Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg  
 675 680 685

TCA TAT ACC CGG GAT TCT TAC AAA ATG CCC GCA ATG GCT GAT AAC ATT 2112  
 Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile  
 690 695 700

CAA GAC CTC CTC CAT TTC TCC CCC CAA ATG TTC TCC ATG AAC GTC CAC 2160  
 Glu Asp Leu Leu His Phe Cys Arg Glu Met Phe Ser Met Lys Val Asp  
 705 710 715 720

AAC CTC GAA TAC CGG CTT CTC ACT GCC ATT GTG ATC TTC TCG GAC CGG 2208  
 Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val He Phe Ser Asp Arg  
 725 730 735

CGC CCC CTC GAG AAC CCC CAA CTA CTC GAA CGG ATC CAG ACC TAC TAC 2256  
 Pro Glu Leu Glu Lys Ala Glu Leu Val Glu Ala Ile Glu Ser Tyr Tyr  
 740 745 750

ATC GAC ACC CTA CCC ATT TAT ATA CTC AAC CGG CAC TCC GGC GAC TCA 2304  
 Ile Asp Thr Leu Arg Ile Tyr He Leu Asn Arg His Cys Gly Asp Ser  
 755 760 765

ATC AGC CTC CTC TTC TAC GCA AAC CGC CTC CTC TCC ATC CTC ACC GAG CTC 2352  
 Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu  
 770 775 780

CGT ACC CTG CGG AAC CAG AAC CGC GAC ATG TGT TTC TCA CTA AAC CTC 2400  
 Arg Thr Leu Gly Asn Glu Asn Ala Glu Met Cys Phe Ser Leu Lys Leu  
 785 790 795 800

AAA AAC CCC AAA CTC CCC AAC TTC CTC GAG GAC ATC TCG GAC GTT CAT 2448  
 Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His  
 805 810 815

GCC ATC CGG CCA TCG GTC CAG TCG CAC CTT CAG ATT ACC CAC CAG GAC 2496  
 Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu  
 820 825 830

AAC CAG CCT CTC GAC CGG CCT CAC CCT ATC CGG CCA TCG CCT CCC CCC 2514  
 Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly  
 835 840 845

CCC ATT ACC CCC CCC ATT GAT TCC GAC TCT CCC TCC ACT TCG CCC CCC 2592  
 Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala  
 850 855 860

GCA GCC CCC CCC CAC CAT CAC CCT CAC CCT CAG CCC CAG CCC CAA CCC 2610  
 Ala Ala Ala Ala Gln His Glu Pro Gln Pro Gln Pro Gln Pro Gln Pro  
 865 870 875 880

TCC TCC CTG ACC CAG AAC CAT TCC CAG CAC CAC ACA CAG CCC CAC CTA 2688  
 Ser Ser Leu Thr Gln Asn Asp Ser Gln His Glu Thr Gln Pro Gln Leu  
 885 890 895

CAA CCT CAG CTA CCA CCT CAG CTC CAA CCT CAA CTC CAA CCC CAG CTC 2736  
 Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu  
 900 905 910

CAA CCA CAG CCT CAG ACC CAA CTC CAC CCA CAG ATT CAA CCA CAG CCA 2784  
 Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro  
 915 920 925

CAC CTC CTT CCC CTC TCC CCT CCC CTC CCC CCC TCC CTA ACC CCA CCT 2832  
 Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro  
 930 935 940

CCT TCC TTG TCC CCC CTC ACT ACC AGC AGC GAA TAC ATG CCC GGA ACT 2880  
 Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser  
 945 950 955 960

CCC CCC ATA CGA CCC ATC ACC CCC GCA ACC ACC ACC ACT ATC ACC CCT 2928  
 Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala  
 965 970 975

CCC GTT ACC CCT ACC TCC ACC ACA TCA CGG CTC CGG ATG CCC AAC GCA 2976  
 Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly  
 980 985 990

CTT CGA CTC CCT CTT CGG GTC CCC CCC AAC CTC ACC ATC TAT CCC AAC 3024  
 Val Gly Val Gly Val Gly Gly Val Gly Asn Val Ser Met Tyr Ala Asn  
 995 1000 1005

CCC CAG ACC CCC ATC CCC TTC ATC CCT CTA CGG CTC CAT TCG CAC CAA 3072  
 Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln  
 1010 1015 1020

CAC CAG CCT ATC CCC GCA CTC CCC CCT AAC TCC GAG CAC TCC ACC ACT 3120  
 Glu Glu Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr  
 1025 1030 1035 1040

GCA TAG  
Ala

3126

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Ser Lys Cln Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser  
 1           5       10       15

Ser Val Leu Ala Cln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr  
 20          25       30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu  
 35          40       45

Ala Val Ala Ser Cln Ser Asp Ser Lys Cln Arg Arg Leu Leu Val Asp  
 50          55       60

Phe Pro Lys Gly Ser Val Ser Asn Ala Cln Cln Pro Asp Leu Ser Lys  
 65          70       75       80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys  
 85          90       95

Val Met Gly Asn Asp Leu Gly Phe Pro Cln Cln Gly Cln Ile Ser Leu  
 100       105       110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn  
 115       120       125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser  
 130       135       140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His  
 145       150       155       160

Ser Asp Val Ser Ser Glu Glu Cln His Leu Lys Gly Cln Thr Gly Thr  
 165       170       175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Cln Ser Thr Phe Asp  
 180       185       190

Ile Leu Cln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr  
 195       200       205

Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu  
 210            215            220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn  
 225            230            235            240

Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys  
 245            250            255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr  
 260            265            270

Leu Pro Glu Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr  
 275            280            285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala  
 290            295            300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser  
 305            310            315            320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met  
 325            330            335

Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn  
 340            345            350

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln  
 355            360            365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro  
 370            375            380

Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro  
 385            390            395            400

Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro  
 405            410            415

Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp  
 420            425            430

Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys  
 435            440            445

Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys  
 450            455            460

Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln  
 465            470            475            480

Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys  
 485            490            495

Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala  
 500            505            510

Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly  
 515            520            525

Gly Asn Gly Ser Leu Ala Ser Gly Gly Gln Asp Phe Val Lys Lys  
 530            535            540

Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile  
 545            550            555            560

Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile  
 565            570            575

Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp  
 580            585            590

Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile  
 595            600            605

Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg  
 610            615            620

His Ile Thr Glu Ile Thr Ile Leu Thr Val Glu Leu Ile Val Glu Phe  
 625            630            635            640

Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile  
 645            650            655

Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala  
 660            665            670

Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg  
 675            680            685

Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile  
 690            695            700

Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp  
 705            710            715            720

Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg  
 725            730            735

Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr  
 740            745            750

Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser  
 755            760            765

Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu  
 770            775            780

Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu  
 785        790        795        800

Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His  
 805        810        815

Ala Ile Pro Pro Ser Val Gin Ser His Leu Gin Ile Thr Gin Glu Glu  
 820        825        830

Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly  
 835        840        845

Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala  
 850        855        860

Ala Ala Ala Ala Glu His Gin Pro Glu Pro Glu Pro Glu Pro Glu Pro  
 865        870        875        880

Ser Ser Leu Thr Gin Asn Asp Ser Glu His Gin Thr Glu Pro Glu Leu  
 885        890        895

Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu  
 900        905        910

Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro  
 915        920        925

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro  
 930        935        940

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser  
 945        950        955        960

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala  
 965        970        975

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly  
 980        985        990

Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn  
 995        1000        1005

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln  
 1010        1015        1020

Gln Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr  
 1025        1030        1035        1040

Ala

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

## (iv) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Modified Ecdysone Response Element"  
 /note = "N at position 7 is 0 up to 5 nucleotides,  
 with 1 nucleotide being especially preferred."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

RCBNINMTCN NCY

13

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

## (iv) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Modified Ecdysone Response Element"  
 /note = "N at position 7 can be 0 up to 5  
 nucleotides, with 1 nucleotide being preferred."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

RGNNCANKNN VCY

13

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGTCCGATGT TCT 13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Ecdysone Response Element"  
/note= "N at position 7 can be 0 up to 5  
nucleotides, with 3 nucleotides being preferred."

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:13:

RGBNNNNRGB NN 13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACAAACCCC TCACCTGTCC ATCTCTCAAG CTGTTTCTTT CGACCCACC 49

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(i) SEQUENCE DESCRIPTION: SEQ ID NO:15:

G T A C T C C C C C G C C T A T G C G G G G G C T A T G C T A A T C C T A G G G G G G G G C C A      53

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(i) SEQUENCE DESCRIPTION: SEQ ID NO:16:

G T A C T C C C C C G C C T A A C C G A T T A G C C C C C G C C C C C A T A G C C C C G G G G G G G C C A      53

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(i) SEQUENCE DESCRIPTION: SEQ ID NO:17:

A G C T C G A T C C A C A A C T C C A T T C T T T C C T G C A A      34

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCTTTCA~~G~~ AAGACAACAA TCCACTTCTC CATCC 35